



IFWO

RAW SEQUENCE LISTING

DATE: 09/09/2004

PATENT APPLICATION: US/10/779,399

TIME: 09:54:51

Input Set : A:\SeqListing.ST25.txt

Output Set: N:\CRF4\09092004\J779399.raw

3 <110> APPLICANT: Uckun, Fatih M.
 5 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF THE BTK KINASE DOMAIN
 7 <130> FILE REFERENCE: 12152.118USW1
 9 <140> CURRENT APPLICATION NUMBER: US 10/779,399
 10 <141> CURRENT FILING DATE: 2004-02-13
 12 <150> PRIOR APPLICATION NUMBER: PCT/US02/26200
 13 <151> PRIOR FILING DATE: 2002-08-15
 15 <150> PRIOR APPLICATION NUMBER: US 60/312,597
 16 <151> PRIOR FILING DATE: 2001-08-15
 18 <150> PRIOR APPLICATION NUMBER: US 60/339,206
 19 <151> PRIOR FILING DATE: 2001-12-07
 21 <160> NUMBER OF SEQ ID NOS: 7
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 659
 27 <212> TYPE: PRT
 28 <213> ORGANISM: Homo sapiens
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 36 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
 37 20 25 30
 40 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
 41 35 40 45
 44 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
 45 50 55 60
 48 Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
 49 65 70 75 80
 52 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
 53 85 90 95
 56 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
 57 100 105 110
 60 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
 61 115 120 125
 64 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
 65 130 135 140
 68 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
 69 145 150 155 160
 72 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
 73 165 170 175
 76 Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
 77 180 185 190
 80 Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala



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84 Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
85      210          215          220
88 Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
89 225          230          235          240
92 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
93          245          250          255
96 Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
97          260          265          270
100 Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
101          275          280          285
104 Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
105          290          295          300
108 Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
109 305          310          315          320
112 Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
113          325          330          335
116 Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
117          340          345          350
120 Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
121          355          360          365
124 Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
125          370          375          380
128 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
129 385          390          395          400
132 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
133          405          410          415
136 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
137          420          425          430
140 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
141          435          440          445
144 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
145          450          455          460
148 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
149 465          470          475          480
152 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
153          485          490          495
156 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
157          500          505          510
160 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
161          515          520          525
164 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
165          530          535          540
168 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
169 545          550          555          560
172 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
173          565          570          575
176 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
177          580          585          590

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180 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
181      595      600      605
184 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
185      610      615      620
188 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
189 625      630      635      640
192 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
193      645      650      655
196 Glu Glu Ser
200 <210> SEQ ID NO: 2
201 <211> LENGTH: 659
202 <212> TYPE: PRT
203 <213> ORGANISM: Murine
205 <400> SEQUENCE: 2
207 Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
208 1      5      10      15
211 Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
212      20      25      30
215 Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
216      35      40      45
219 Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
220      50      55      60
223 Glu Thr Val Ile Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
224 65      70      75      80
227 Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
228      85      90      95
231 Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
232      100     105     110
235 Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Pro Trp Ile His Gln Leu
236      115     120     125
239 Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
240      130     135     140
243 Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
244 145     150     155     160
247 Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
248      165     170     175
251 Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
252      180     185     190
255 Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Thr Ala
256      195     200     205
259 Ala Pro Ile Ser Thr Thr Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
260      210     215     220
263 Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Glu Glu
264 225     230     235     240
267 Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
268      245     250     255
271 Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Ile Thr Glu Ala
272      260     265     270
275 Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg

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276          275          280          285
279 Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
280      290          295          300
283 Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
284 305          310          315          320
287 Ala Lys Ser Thr Gly Glu Pro Gln Gly Val Ile Arg His Tyr Val Val
288          325          330          335
291 Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
292          340          345          350
295 Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
296          355          360          365
299 Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Lys Gln Asn Lys Asn Ala
300          370          375          380
303 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
304 385          390          395          400
307 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
308          405          410          415
311 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
312          420          425          430
315 Arg Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
316          435          440          445
319 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
320          450          455          460
323 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
324 465          470          475          480
327 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
328          485          490          495
331 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
332          500          505          510
335 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
336          515          520          525
339 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
340          530          535          540
343 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
344 545          550          555          560
347 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
348          565          570          575
351 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
352          580          585          590
355 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
356          595          600          605
359 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
360          610          615          620
363 Arg Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
364 625          630          635          640
367 Arg Pro Ser Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
368          645          650          655
371 Glu Glu Ser
375 <210> SEQ ID NO: 3

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376 <211> LENGTH: 263
377 <212> TYPE: PRT
378 <213> ORGANISM: Homo sapiens
380 <400> SEQUENCE: 3
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386 Phe Gly Val Val Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala
387 20 25 30
390 Ile Lys Met Ile Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu
391 35 40 45
394 Glu Ala Lys Val Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu
395 50 55 60
398 Tyr Gly Val Cys Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr
399 65 70 75 80
402 Met Ala Asn Gly Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg
403 85 90 95
406 Phe Gln Thr Gln Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala
407 100 105 110
410 Met Glu Tyr Leu Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala
411 115 120 125
414 Arg Asn Cys Leu Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe
415 130 135 140
418 Gly Leu Ser Arg Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly
419 145 150 155 160
422 Ser Lys Phe Pro Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser
423 165 170 175
426 Lys Phe Ser Ser Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp
427 180 185 190
430 Glu Ile Tyr Ser Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser
431 195 200 205
434 Glu Thr Ala Glu His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His
435 210 215 220
438 Leu Ala Ser Glu Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu
439 225 230 235 240
442 Lys Ala Asp Glu Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu
443 245 250 255
446 Asp Val Met Asp Glu Glu Ser
447 260
450 <210> SEQ ID NO: 4
451 <211> LENGTH: 263
452 <212> TYPE: PRT
453 <213> ORGANISM: Murine
455 <400> SEQUENCE: 4
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458 1 5 10 15
461 Phe Gly Val Val Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala
462 20 25 30
465 Ile Lys Met Ile Arg Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu
466 35 40 45

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VERIFICATION SUMMARY

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